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SEQUENCE LISTING

<110> NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY
AMERSHAM BIOSCIENCES K.K.

<120> METHOD OF DETECTING BONE PAGET'S DISEASE

<130> YCT-882

<150> JP2002-323438

<151> 2002-11-07

<160> 70

<170> PatentIn version 3.1

<210> 1

<211> 2649

<212> DNA

<213> Homo sapiens

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<222> (1)..(2649)

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Val Leu Gly Phe Thr Ala Ala Ser Trp Leu Ile Ala Pro Arg Val Ala

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Glu Leu Ser Glu Arg Lys Arg Arg Gly Ser Ser Leu Cys Ser Tyr Tyr

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Gln Asp Leu Gln Gly Pro Pro Leu Pro Glu Ala Ala Pro Gly Ile Thr			
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Ser Phe Arg Ser Ser Pro Trp Gln Gln Pro Pro Pro Leu Gln Gln Arg			
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Arg Arg Gly Arg Glu Pro Glu Gly Ala Thr Gly Leu Pro Gly Ala Pro			
115	120	125	
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Gly Ala Ala Ala Pro Ser Ala Arg Pro Arg Asp Phe Leu Tyr Val Gly			
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Arg Thr Trp Ala Arg Phe Ile Pro Gly Arg Val Glu Phe Phe Ser Ser			
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Ser Lys Ile His Ala Ala Ile Thr Leu His Pro Asn Lys Arg Pro Ala			
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Lys Leu Ser Asn Thr Glu Val Ser Lys Glu Asp Gln Gln Leu Gly Val			
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515 520 525	
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Phe Glu Asn Met Cys Leu Ile Pro Lys Gln Asn Val Lys Leu Val Ile			
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770	775	780	
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Leu Ser			2649

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145 150 155 160

Gly Ala Ala Ala Pro Ser Ala Arg Pro Arg Asp Phe Leu Tyr Val Gly
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Val Met Thr Ala Gln Lys Tyr Leu Gly Ser Arg Ala Leu Ala Ala Gln
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Ala Leu Pro Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe

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755 760 765

Ser Lys Lys Thr Gly Phe Trp Arg Asp Tyr Gly Tyr Gly Ile Thr Cys
770 775 780

Ile Tyr Lys Ser Asp Leu Leu Gly Ala Gly Gly Phe Asp Thr Ser Ile
785 790 795 800

Gln Gly Trp Gly Leu Glu Asp Val Asp Leu Tyr Asn Lys Val Ile Leu
805 810 815

Ser Gly Leu Arg Pro Phe Arg Ser Gln Glu Val Gly Val Val His Ile

820

825

830

Phe His Pro Val His Cys Asp Pro Asn Leu Asp Pro Lys Gln Tyr Lys

835

840

845

Met Cys Leu Gly Ser Lys Ala Ser Thr Phe Ala Ser Thr Met Gln Leu

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Leu Ser

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Ala Val Gly Ile Ser Leu Gly Phe Thr Leu Ser Leu Leu Ser Val Thr

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Val Gln Pro Gly Ala Glu Arg Glu Lys Pro Gly Ala Gly Glu Gly Ala			
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ggg gag aat tgg gag ccg cgc gtc ttg ccc tac cac cct gca cag ccc			288
Gly Glu Asn Trp Glu Pro Arg Val Leu Pro Tyr His Pro Ala Gln Pro			
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Gly Gln Ala Ala Lys Lys Ala Val Arg Thr Arg Tyr Ile Ser Thr Glu			
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ctg ggc atc agg cag agg ctg ctg gtg gcg gtg ctg acc tct cag acc			384
Leu Gly Ile Arg Gln Arg Leu Leu Val Ala Val Leu Thr Ser Gln Thr			
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acg ctg ccc acg ctg ggc gtg gcc gtg aac cgc acg ctg ggg cac cgg			432
Thr Leu Pro Thr Leu Gly Val Ala Val Asn Arg Thr Leu Gly His Arg			
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cct ggc atg gca gtg gtg acg ctg ggc gag gag cga ccc att gga cac			528
Pro Gly Met Ala Val Val Thr Leu Gly Glu Glu Arg Pro Ile Gly His			
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ctg cac ctg gcg ctg cgc cac ctg ctg gag cag cac ggc gac gac ttt			576
Leu His Leu Ala Leu Arg His Leu Leu Glu Gln His Gly Asp Asp Phe			
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gac tgg ttc ttc ctg gtg cct gac acc acc tac acc gag gcg cac ggc			624
Asp Trp Phe Phe Leu Val Pro Asp Thr Thr Tyr Thr Glu Ala His Gly			
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Leu Ala Arg Leu Thr Gly His Leu Ser Leu Ala Ser Ala Ala His Leu			
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Tyr Leu Gly Arg Pro Gln Asp Phe Ile Gly Gly Glu Pro Thr Pro Gly			

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Arg Tyr Cys His Gly Gly Phe Gly Val Leu Leu Ser Arg Met Leu Leu				
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Gln Gln Leu Arg Pro His Leu Glu Gly Cys Arg Asn Asp Ile Val Ser				
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Ala Arg Pro Asp Glu Trp Leu Gly Arg Cys Ile Leu Asp Ala Thr Gly				
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Val Gly Cys Thr Gly Asp His Glu Gly Val His Tyr Ser His Leu Glu				
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Ala Leu Thr Ala His Pro Val Arg Asp Pro Val His Met Tyr Gln Leu				
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His Lys Ala Phe Ala Arg Ala Glu Leu Glu Arg Thr Tyr Gln Glu Ile				
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Gln Glu Leu Gln Trp Glu Ile Gln Asn Thr Ser His Leu Ala Val Asp				
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Pro Ala Ser Arg Phe Glu Val Leu Arg Trp Asp Tyr Phe Thr Glu Gln				
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His Ala Phe Ser Cys Ala Asp Gly Ser Pro Arg Cys Pro Leu Arg Gly				
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Ala Asp Arg Ala Asp Val Ala Asp Val Leu Gly Thr Ala Leu Glu Glu				
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Pro Met His Phe Gln Ala Phe His Pro Ala Val Ala Pro Pro Gln Gly			
645	650	655	
cct ggg ccc cca gag ctg ggc cgt gac act ggc cgc ttt gat cgc cag			2016
Pro Gly Pro Pro Glu Leu Gly Arg Asp Thr Gly Arg Phe Asp Arg Gln			
660	665	670	
gca gcc agc gag gcc tgc ttc tac aac tcc gac tac gtg gca gcc cgt			2064
Ala Ala Ser Glu Ala Cys Phe Tyr Asn Ser Asp Tyr Val Ala Ala Arg			
675	680	685	
ggg cgc ctg gcg gca gcc tca gaa caa gaa gag gag ctg ctg gag agc			2112
Gly Arg Leu Ala Ala Ser Glu Gln Glu Glu Leu Leu Glu Ser			
690	695	700	
ctg gat gtg tac gag ctg ttc ctc cac ttc tcc agt ctg cat gtg ctg			2160
Leu Asp Val Tyr Glu Leu Phe Leu His Phe Ser Ser Leu His Val Leu			
705	710	715	720
cgg gcg gtg gag ccg gcg ctg ctg cag cgc tac cgg gcc cag acg tgc			2208
Arg Ala Val Glu Pro Ala Leu Leu Gln Arg Tyr Arg Ala Gln Thr Cys			
725	730	735	
agc gcg agg ctc agt gag gac ctg tac cac cgc tgc ctc cag agc gtg			2256
Ser Ala Arg Leu Ser Glu Asp Leu Tyr His Arg Cys Leu Gln Ser Val			
740	745	750	
ctt gag ggc ctc ggc tcc cga acc cag ctg gcc atg cta ctc ttt gaa			2304
Leu Glu Gly Leu Gly Ser Arg Thr Gln Leu Ala Met Leu Leu Phe Glu			
755	760	765	
cag gag cag ggc aac agc acc tga			2328
Gln Gln Gly Asn Ser Thr			
770	775		

<210> 4
 <211> 775
 <212> PRT
 <213> Homo sapiens

<400> 4

Met Arg Ala Ser Leu Leu Leu Ser Val Leu Arg Pro Ala Gly Pro Val
1 5 10 15

Ala Val Gly Ile Ser Leu Gly Phe Thr Leu Ser Leu Leu Ser Val Thr
20 25 30

Trp Val Glu Glu Pro Cys Gly Pro Gly Pro Pro Gln Pro Gly Asp Ser
35 40 45

Glu Leu Pro Pro Arg Gly Asn Thr Asn Ala Ala Arg Arg Pro Asn Ser
50 55 60

Val Gln Pro Gly Ala Glu Arg Glu Lys Pro Gly Ala Gly Glu Gly Ala
65 70 75 80

Gly Glu Asn Trp Glu Pro Arg Val Leu Pro Tyr His Pro Ala Gln Pro
85 90 95

Gly Gln Ala Ala Lys Lys Ala Val Arg Thr Arg Tyr Ile Ser Thr Glu
100 105 110

Leu Gly Ile Arg Gln Arg Leu Leu Val Ala Val Leu Thr Ser Gln Thr
115 120 125

Thr Leu Pro Thr Leu Gly Val Ala Val Asn Arg Thr Leu Gly His Arg
130 135 140

Leu Glu Arg Val Val Phe Leu Thr Gly Ala Arg Gly Arg Arg Ala Pro

145 150 155 160

Pro Gly Met Ala Val Val Thr Leu Gly Glu Glu Arg Pro Ile Gly His
165 170 175

Leu His Leu Ala Leu Arg His Leu Leu Glu Gln His Gly Asp Asp Phe
180 185 190

Asp Trp Phe Phe Leu Val Pro Asp Thr Thr Tyr Thr Glu Ala His Gly
195 200 205

Leu Ala Arg Leu Thr Gly His Leu Ser Leu Ala Ser Ala Ala His Leu
210 215 220

Tyr Leu Gly Arg Pro Gln Asp Phe Ile Gly Gly Glu Pro Thr Pro Gly
225 230 235 240

Arg Tyr Cys His Gly Gly Phe Gly Val Leu Leu Ser Arg Met Leu Leu
245 250 255

Gln Gln Leu Arg Pro His Leu Glu Gly Cys Arg Asn Asp Ile Val Ser
260 265 270

Ala Arg Pro Asp Glu Trp Leu Gly Arg Cys Ile Leu Asp Ala Thr Gly
275 280 285

Val Gly Cys Thr Gly Asp His Glu Gly Val His Tyr Ser His Leu Glu
290 295 300

Leu Ser Pro Gly Glu Pro Val Gln Glu Gly Asp Pro His Phe Arg Ser
305 310 315 320

Ala Leu Thr Ala His Pro Val Arg Asp Pro Val His Met Tyr Gln Leu
325 330 335

His Lys Ala Phe Ala Arg Ala Glu Leu Glu Arg Thr Tyr Gln Glu Ile
340 345 350

Gln Glu Leu Gln Trp Glu Ile Gln Asn Thr Ser His Leu Ala Val Asp
355 360 365

Gly Asp Arg Ala Ala Ala Trp Pro Val Gly Ile Pro Ala Pro Ser Arg
370 375 380

Pro Ala Ser Arg Phe Glu Val Leu Arg Trp Asp Tyr Phe Thr Glu Gln
385 390 395 400

His Ala Phe Ser Cys Ala Asp Gly Ser Pro Arg Cys Pro Leu Arg Gly
405 410 415

Ala Asp Arg Ala Asp Val Ala Asp Val Leu Gly Thr Ala Leu Glu Glu
420 425 430

Leu Asn Arg Arg Tyr His Pro Ala Leu Arg Leu Gln Lys Gln Gln Leu
435 440 445

Val Asn Gly Tyr Arg Arg Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr
450 455 460

Leu Asp Leu Gln Leu Glu Ala Leu Thr Pro Gln Gly Gly Arg Arg Pro
465 470 475 480

Leu Thr Arg Arg Val Gln Leu Leu Arg Pro Leu Ser Arg Val Glu Ile
485 490 495

Leu Pro Val Pro Tyr Val Thr Glu Ala Ser Arg Leu Thr Val Leu Leu
500 505 510

Pro Leu Ala Ala Ala Glu Arg Asp Leu Ala Pro Gly Phe Leu Glu Ala
515 520 525

Phe Ala Thr Ala Ala Leu Glu Pro Gly Asp Ala Ala Ala Leu Thr
530 535 540

Leu Leu Leu Leu Tyr Glu Pro Arg Gln Ala Gln Arg Val Ala His Ala
545 550 555 560

Asp Val Phe Ala Pro Val Lys Ala His Val Ala Glu Leu Glu Arg Arg
565 570 575

Phe Pro Gly Ala Arg Val Pro Trp Leu Ser Val Gln Thr Ala Ala Pro
580 585 590

Ser Pro Leu Arg Leu Met Asp Leu Leu Ser Lys Lys His Pro Leu Asp
595 600 605

Thr Leu Phe Leu Leu Ala Gly Pro Asp Thr Val Leu Thr Pro Asp Phe
610 615 620

Leu Asn Arg Cys Arg Met His Ala Ile Ser Gly Trp Gln Ala Phe Phe
625 630 635 640

Pro Met His Phe Gln Ala Phe His Pro Ala Val Ala Pro Pro Gln Gly
645 650 655

Pro Gly Pro Pro Glu Leu Gly Arg Asp Thr Gly Arg Phe Asp Arg Gln
660 665 670

Ala Ala Ser Glu Ala Cys Phe Tyr Asn Ser Asp Tyr Val Ala Ala Arg
675 680 685

Gly Arg Leu Ala Ala Ala Ser Glu Gln Glu Glu Glu Leu Leu Glu Ser
690 695 700

Leu Asp Val Tyr Glu Leu Phe Leu His Phe Ser Ser Leu His Val Leu
705 710 715 720

Arg Ala Val Glu Pro Ala Leu Leu Gln Arg Tyr Arg Ala Gln Thr Cys
725 730 735

Ser Ala Arg Leu Ser Glu Asp Leu Tyr His Arg Cys Leu Gln Ser Val

740

745

750

Leu Glu Gly Leu Gly Ser Arg Thr Gln Leu Ala Met Leu Leu Phe Glu
755 760 765

Gln Glu Gln Gly Asn Ser Thr
770 775

<210> 5
<211> 1669
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (41)..(1024)
<223>

<400> 5
ctgcgagcgc ctgccccatg cgccggccgcc tctccgcacg atg ttc ccc tcg cgg 55
Met Phe Pro Ser Arg
1 5
agg aaa gcg gcg cag ctg ccc tgg gag gac ggc agg tcc ggg ttg ctc 103
Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp Gly Arg Ser Gly Leu Leu
10 15 20
tcc ggc ggc ctc cct cgg aag tgt tcc gtc ttc cac ctg ttc gtg gcc 151
Ser Gly Leu Pro Arg Lys Cys Ser Val Phe His Leu Phe Val Ala
25 30 35
tgc ctc tcg ctg ggc ttc ttc tcc cta ctc tgg ctg cag ctc agc tgc 199
Cys Leu Ser Leu Gly Phe Phe Ser Leu Leu Trp Leu Gln Leu Ser Cys
40 45 50
tct ggg gac gtg gcc cgg gca gtc agg gga caa ggg cag gag acc tcg 247
Ser Gly Asp Val Ala Arg Ala Val Arg Gly Gln Gly Gln Glu Thr Ser
55 60 65

ggc cct ccc cgc gcc tgc ccc cca gag ccg ccc cct gag cac tac tgg gaa		295	
Gly Pro Pro Arg Ala Cys Pro Pro Glu Pro Pro Glu His Trp Glu			
70	75	80	85
gaa gac gca tcc tgg ggc ccc cac cgc ctg gca gtg ctg gtg ccc ttc		343	
Glu Asp Ala Ser Trp Gly Pro His Arg Leu Ala Val Leu Val Pro Phe			
90	95	100	
cgc gaa cgc ttc gag gag ctc ctg gtc ttc gtg ccc cac atg cgc cgc		391	
Arg Glu Arg Phe Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg			
105	110	115	
ttc ctg agc agg aag aag atc cgg cac cac atc tac gtg ctc aac cag		439	
Phe Leu Ser Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln			
120	125	130	
gtg gac cac ttc agg ttc aac cgg gca gcg ctc atc aac gtg ggc ttc		487	
Val Asp His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe			
135	140	145	
ctg gag agc agc aac agc acg gac tac att gcc atg cac gac gtt gac		535	
Leu Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala Met His Asp Val Asp			
150	155	160	165
ctg ctc cct ctc aac gag gag ctg gac tat ggc ttt cct gag gct ggg		583	
Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly Phe Pro Glu Ala Gly			
170	175	180	
ccc ttc cac gtg gcc tcc ccg gag ctc cac cct ctc tac cac tac aag		631	
Pro Phe His Val Ala Ser Pro Glu Leu His Pro Leu Tyr His Tyr Lys			
185	190	195	
acc tat gtc ggc ggc atc ctg ctg ctc tcc aag cag cac tac cgg ctg		679	
Thr Tyr Val Gly Gly Ile Leu Leu Ser Lys Gln His Tyr Arg Leu			
200	205	210	
tgc aat ggg atg tcc aac cgc ttc tgg ggc tgg ggc cgc gag gac gac		727	
Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp Gly Arg Glu Asp Asp			
215	220	225	
gag ttc tac cgg cgc att aag gga gct ggg ctc cag ctt ttc cgc ccc		775	
Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu Gln Leu Phe Arg Pro			
230	235	240	245
tcg gga atc aca act ggg tac aag aca ttt cgc cac ctg cac gac cca		823	
Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe Arg His Leu His Asp Pro			
250	255	260	
gcc tgg cgg aag agg gac cag aag cgc atc gca gct caa aaa cag gag		871	

Ala Trp Arg Lys Arg Asp Gln Lys Arg Ile Ala Ala Gln Lys Gln Glu			
265	270	275	
cag ttc aag gtg gac agg gag gga ggc ctg aac act gtg aag tac cat			919
Gln Phe Lys Val Asp Arg Glu Gly Gly Leu Asn Thr Val Lys Tyr His			
280	285	290	
gtg gct tcc cgc act gcc ctg tct gtg ggc ggg gcc ccc tgc act gtc			967
Val Ala Ser Arg Thr Ala Leu Ser Val Gly Gly Ala Pro Cys Thr Val			
295	300	305	
ctc aac atc atg ttg gac tgt gac aag acc gcc aca ccc tgg tgc aca			1015
Leu Asn Ile Met Leu Asp Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr			
310	315	320	325
ttc agc tga gctggatgga cagtgaggaa gcctgtacct acaggccata			1064
Phe Ser			
ttgcgtcaggc tcaggacaag gcctcaggic gggggccag ctgtgacagg atgtggatgt			1124
gccaggacca agacagcaag ctacgcaatt gcagccaccc ggccgc当地 agcaggcttgg			1184
gctggccag gacacgttggg gtgcctggga cgctgttgtc catgcacagt gatcagagag			1244
aggcttgggtt gtgtcctgtc cgggaccccc cctgccttcc tgctcacccct actctgaccc			1304
ccttcacgtt cccaggccctg tggtagtgg ggagggctga acaggacaac ctctcatcac			1364
ccccactttt gttcccttcct gctgggcgtc ctctgtcaga gacacagtgtt agggccatgt			1424
cagctggcgtt aggtggcagt tggcccttgtt gagggtagg actttagaaaa ccagagcaca			1484
agccccacag agggggaaaca gccagcacccg ctcttagtgg ttgttgccat gccc当地atgt			1544
ggcccttagtgg ttgtccatgtt ttgtatttt tcgaaagaaa cttagaatgtt ggatttttaa			1604
gtgatatctt ctgtttttt aaatgtatgc acctaaatgtt aactttcaaa aagtaaaaaaa			1664
aaaaaa			1669

<210> 6
 <211> 327
 <212> PRT
 <213> Homo sapiens

<400> 6

Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp Gly			
1	5	10	15

Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser Val Phe

20	25	30
His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser Leu Leu Trp		
35	40	45
Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala Val Arg Gly Gln		
50	55	60
Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys Pro Pro Glu Pro Pro		
65	70	75
80		
Pro Glu His Trp Glu Glu Asp Ala Ser Trp Gly Pro His Arg Leu Ala		
85	90	95
Val Leu Val Pro Phe Arg Glu Arg Phe Glu Glu Leu Leu Val Phe Val		
100	105	110
Pro His Met Arg Arg Phe Leu Ser Arg Lys Lys Ile Arg His His Ile		
115	120	125
Tyr Val Leu Asn Gln Val Asp His Phe Arg Phe Asn Arg Ala Ala Leu		
130	135	140
Ile Asn Val Gly Phe Leu Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala		
145	150	155
160		
Met His Asp Val Asp Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly		
165	170	175

Phe Pro Glu Ala Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro
180 185 190

Leu Tyr His Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys
195 200 205

Gln His Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp
210 215 220

Gly Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu
225 230 240

Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe Arg
245 250 255

His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg Ile Ala
260 265 270

Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly Gly Leu Asn
275 280 285

Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu Ser Val Gly Gly
290 295 300

Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp Cys Asp Lys Thr Ala
305 310 315 320

Thr Pro Trp Cys Thr Phe Ser
325

<210> 7
<211> 26
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 5' primer for PCR (K3)

<400> 7
cccaagcttg ccgaggggga gcccgaa 26

<210> 8
<211> 29
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 3' primer for PCR (K3)

<400> 8
gctctagact gtcaggagag agttcgatt 29

<210> 9
<211> 25
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 5' primer for PCR (K3)

<400> 9
atggctgtgc gcctcgcgg cccgt 25

<210> 10

<211> 25

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for PCR (K3)

<400> 10

cgtcccccgtt gccgttgtgg ctact

25

<210> 11

<211> 25

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 5' primer for PCR (K3)

<400> 11

agttagccaca acggcagcgg ggacg

25

<210> 12

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for PCR (K3)

<400> 12

tcaaggagaga gttcgatgtt acct

24

<210> 13

<211> 28

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 5' primer for PCR (K11)

<400> 13

ggaattccgg ccaggccgcc aaaaaggc

28

<210> 14

<211> 30

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for PCR (K11)

<400> 14

cgggatcctc aggtgcgtt gccctgctcc

30

<210> 15

<211> 16

<212> PRT

<213> Artificial

<220>

<223> Description of Artificial Sequence: synthesised substance for assay

<400> 15

Val Leu Pro Gln Glu Glu Gly Ser Gly Gly Gln Leu Val Thr

1

5

10

15

<210> 16

<211> 20

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (K3 exon 1)

<400> 16

cgacagccca gcgagcgicc

20

<210> 17

<211> 22

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (K3 exon 1)

<400> 17

ggagactggc aggctggaaa gc

22

<210> 18

<211> 20

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Primer for sequencing (K3 exon 1)

<400> 18

agggggagcc cgaggaggag

20

<210> 19

<211> 20

<212> DNA

<213> Artificial

<220>
<223> Description of Artificial Sequence: Primer for sequencing (K3 exon 1)

<400> 19
ctccctcccg ggctccccct 20

<210> 20
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (K3 exon 2)

<400> 20
gagacatagt aattgttgcc ttcttt 27

<210> 21
<211> 25
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (K3 exon 2)

<400> 21
gtgaacatit tcatcacagc tccat 25

<210> 22
<211> 26
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (K3 exon 3)

<400> 22
tagatgcitt agitttatcgc tggttt 26

<210> 23
<211> 26
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (K3 exon 3)

<400> 23
ttaaaaaagg caaaatgtgt tgcctg 26

<210> 24
<211> 24
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: Primer for sequencing (K3 exon 3)

<400> 24
tctatactca gcagctgaga acca 24

<210> 25
<211> 24
<212> DNA
<213> Artificial

<220>

<223> Description of Artificial Sequence: Primer for sequencing (K3 exon 3)

<400> 25

tggttcttcag ctgcgtgatgta taga

24

<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Primer for sequencing (K3 exon 3)

<400> 26

gaaatgggag ggcacaatga aaag

24

<210> 27

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Primer for sequencing (K3 exon 3)

<400> 27

cttttcattt tgccctcccc ttcc

24

<210> 28

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Primer for sequencing (K3 exon

n 3)

<400> 28

tagccagtat gacccaaagg taac

24

<210> 29

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Primer for sequencing (K3 exon 3)

<400> 29

gttaccctttg ggtcatactg gcta

24

<210> 30

<211> 31

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Primer for sequencing (K3 exon 3)

<400> 30

aggccattca gaagccaaga agtaggagtg g

31

<210> 31

<211> 31

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Primer for sequencing (K3 exon 3)

<400> 31
ccactcctac ttcttggtt ctgaatggcc t 31

<210> 32
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (K11 exon 1)

<400> 32
tcggagactc ctctggctgc t 21

<210> 33
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (K11 exon 1)

<400> 33
tagagcgggc gcagccgatc a 21

<210> 34
<211> 25
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (K11 exon 2)

<400> 34
tttgataagc ttgtgccatc tcctc 25

<210> 35
<211> 25
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (K11 exon 2)

<400> 35
aggatatcgat gggatagctt atcat 25

<210> 36
<211> 24
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (K11 exon 3)

<400> 36
agctcatcac agatcccttc cctt 24

<210> 37
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (K11 exon 1)

<400> 37

actctggcac cccagacct ag 22

<210> 38

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (K11 exon 4)

<400> 38

ttagtggatgg ccgttttc tcat 24

<210> 39

<211> 21

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (K11 exon 4)

<400> 39

gttgtggccat gccacggccc a 21

<210> 40

<211> 23

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Primer for sequencing (K11 exon 4)

<400> 40

tatgtcactg aggccctcagc tct 23

<210> 41
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: Primer for sequencing (K11 exon 4)

<400> 41
agacgtgagg cctcagtgac ata 23

<210> 42
<211> 24
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: primer for sequencing (K11 exon 4)

<400> 42
atgcatttcc aagccttcca cccca 24

<210> 43
<211> 24
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: Primer for sequencing (K11 exon 4)

<400> 43
tgggtggaaag gcgtggaaat gcat 24

<210> 44
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (beta4Gal-T7 exon 1)

<400> 44
tgcgagcgcc tgccccatgc 20

<210> 45
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (beta4Gal-T7 exon 1)

<400> 45
gatggccctcg ggttccaga tt 22

<210> 46
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (beta4Gal-T7 exon 2)

<400> 46
tcctgaccct gtcccgcgct t 21

<210> 47

<211> 20
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (beta4Gal-T7 exon 2)

<400> 47
agggttgccg aggggagagg 20

<210> 48
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (beta4Gal-T7 exon 3)

<400> 48
ctgcccagcc ttgcccaccc t 21

<210> 49
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (beta4Gal-T7 exon 3)

<400> 49
gctctgagca gagcaggcig tc 22

<210> 50
<211> 22

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (beta4Gal-T7 exon 4)

<400> 50

agatgggccg agtgacgc tg ct

22

<210> 51

<211> 21

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (beta4Gal-T7 exon 4)

<400> 51

cicagggcag ccaccgcagc t

21

<210> 52

<211> 22

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (beta4Gal-T7 exon 5)

<400> 52

aaggcagcc tgaccccgac tt

22

<210> 53

<211> 23

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (beta4Gal-T7 exon 5)

<400> 53

atgaccaccc atccgtcccc aat

23

<210> 54

<211> 22

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (beta4Gal-T7 exon 6)

<400> 54

cagcccttag tccgtgcctt tt

22

<210> 55

<211> 23

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (beta4Gal-T7 exon 6)

<220>

<221> misc_feature

<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (beta4Gal-T7 exon 6)

<400> 55

tggcctgttag gtaacaggctt cct 23

<210> 56

<211> 23

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 5' primer for RT-PCR (K3)

<400> 56

cccgagaaaaa gtcctttcatg atg 23

<210> 57

<211> 30

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for RT-PCR (K3)

<400> 57

aactcttcta atttgtcacc tttagatgtag 30

<210> 58

<211> 17

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Probe for RT-PCR (K3)

<400> 58

atgagtggtt catgcgc 17

<210> 59

<211> 20

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 5' primer for RT-PCR (K11)

<400> 59

gctgaactgg aacgcacgta 20

<210> 60

<211> 19

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for RT-PCR (K11)

<400> 60

cggatggtg ctggaatac 19

<210> 61

<211> 20

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Probe for RT-PCR (K11)

<400> 61

agatccagga gttacagtg 20

<210> 62

<211> 18

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 5' primer for RT-PCR (beta4Gal-T7)

<400> 62

cggcgcatta agggagct

18

<210> 63

<211> 21

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for RT-PCR (beta4Gal-T7)

<400> 63

tacccagttg tgattcccg a g

21

<210> 64

<211> 14

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Probe for RT-PCR (beta4Gal-T7)

<400> 64

ctccagcttt tccg

14

<210> 65

<211> 2652

<212> DNA

<213> mouse

<220>

<221> CDS

<222> (1)..(2652)

<223>

<400> 65

atg	gcc	gtg	cgc	tcc	cgc	cgc	cca	tgg	gtg	agc	gtg	gca	ttg	ggg	ttg		48
Met	Ala	Val	Arg	Ser	Arg	Arg	Pro	Trp	Val	Ser	Val	Ala	Leu	Gly	Leu		
1	5				10								15				
gtc	ctg	ggc	ttc	acc	gcc	gcf	tcc	tgg	ctc	atc	gcc	ccc	cgf	gtg	gcc		96
Val	Leu	Gly	Phe	Thr	Ala	Ala	Ser	Trp	Leu	Ile	Ala	Pro	Arg	Val	Ala		
	20				25								30				
gag	ctg	agc	gag	aag	agg	cga	cgc	ggc	tcc	agt	ctt	tgc	tcc	tac	tac		144
Glu	Leu	Ser	Glu	Lys	Arg	Arg	Gly	Ser	Ser	Leu	Cys	Ser	Tyr	Tyr			
	35				40								45				
ggc	cgc	tcg	gct	acc	ggg	ccc	cgc	gcf	gac	gcf	cag	cag	ctg	ctc	ccc		192
Gly	Arg	Ser	Ala	Thr	Gly	Pro	Arg	Ala	Asp	Ala	Gln	Gln	Leu	Leu	Pro		
	50				55								60				
caa	ccc	cag	tcc	cgf	ccg	cgf	cta	gag	cag	tcg	ccg	ccc	cct	gcc	agc		240
Gln	Pro	Gln	Ser	Arg	Pro	Arg	Leu	Glu	Gln	Ser	Pro	Pro	Pro	Ala	Ser		
	65				70								75		80		
cac	gag	ctc	ccc	ggt	cct	cag	cag	ccg	gag	gcf	gcf	ccc	gga	ggt	ccc		288
His	Glu	Leu	Pro	Gly	Pro	Gln	Gln	Pro	Glu	Ala	Ala	Pro	Gly	Gly	Pro		
	85				90								95				
agt	ttt	cgf	agc	ccc	tgg	cag	cag	ccg	gct	ctg	ttg	ccg	cag	agg		336	
Ser	Phe	Arg	Ser	Ser	Pro	Trp	Gln	Gln	Pro	Ala	Leu	Leu	Pro	Gln	Arg		
	100				105								110				
agg	cga	gga	cac	acg	ccc	gaa	ggt	gcf	acg	gcf	ctt	ccc	ggc	gct	ccg		384
Arg	Arg	Gly	His	Thr	Pro	Glu	Gly	Ala	Thr	Ala	Leu	Pro	Gly	Ala	Pro		
	115				120								125				
gct	gcc	aaa	ggg	gaa	cca	gag	gag	gat	ggg	ggc	gcf	gct	gac	cct		432	
Ala	Ala	Lys	Gly	Glu	Pro	Glu	Glu	Asp	Gly	Ala	Ala	Asp	Pro				
	130				135								140				
cgg	aag	ggt	ggc	cgf	ccg	ggg	agc	agc	cac	aac	ggc	agc	ggg	gac	ggg		480
Arg	Lys	Gly	Gly	Arg	Pro	Gly	Ser	Ser	His	Asn	Gly	Ser	Gly	Asp	Gly		
	145				150								155		160		
ggt	gcc	gct	gtc	ccg	acc	tcc	gga	ccc	ggg	gac	ttc	ctg	tac	gtg	ggt		528
Gly	Ala	Ala	Val	Pro	Thr	Ser	Gly	Pro	Gly	Asp	Phe	Leu	Tyr	Val	Gly		
	165				170								175				

gtg atg acc gca cag aag tac ctg ggc agt cgc gcg ctg gcc gcg cag		576	
Val Met Thr Ala Gln Lys Tyr Leu Gly Ser Arg Ala Leu Ala Ala Gln			
180	185	190	
cgg acc tgg gcg cgc ttc atc cct ggc cgc gtg gag ttc ttt tcc agt		624	
Arg Thr Trp Ala Arg Phe Ile Pro Gly Arg Val Glu Phe Phe Ser Ser			
195	200	205	
cag caa tct ccc agt gct gcg ctt ggc cag ccc ccg cca cct ttg cct		672	
Gln Gln Ser Pro Ser Ala Ala Leu Gly Gln Pro Pro Pro Leu Pro			
210	215	220	
gtc atc gcg ctg cca ggg gtc gac gat tcc tac cct ccc cag aaa aag		720	
Val Ile Ala Leu Pro Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys			
225	230	235	240
tcc ttc atg atg aic aag tac atg cac gac cac tat ctg gac aag tat		768	
Ser Phe Met Met Ile Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr			
245	250	255	
gag tgg ttc atg cgc gcc gac gac gat gtc tac atc aaa ggt gat aag		816	
Glu Trp Phe Met Arg Ala Asp Asp Val Tyr Ile Lys Gly Asp Lys			
260	265	270	
tta gaa gaa ttt cta aga tcc cta aat agc agc aag cct ctc tac ctg		864	
Leu Glu Glu Phe Leu Arg Ser Leu Asn Ser Ser Lys Pro Leu Tyr Leu			
275	280	285	
gga cag acg ggc ctg ggc aat act gaa gaa ctt gga aag ctg ggg ctg		912	
Gly Gln Thr Gly Leu Gly Asn Thr Glu Glu Leu Gly Lys Leu Gly Leu			
290	295	300	
gag ccc ggg gag aac ttc tgc atg gga gga cct ggc atg atc ttc agc		960	
Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Met Ile Phe Ser			
305	310	315	320
aga gag gtt ctc agg cgg atg gtg cct cat atc ggc gaa tgc ctc cga		1008	
Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly Glu Cys Leu Arg			
325	330	335	
gag atg tac acc aca cac gaa gac gta gaa gta gga agg tgt gtt cgc		1056	
Glu Met Tyr Thr His Glu Asp Val Glu Val Gly Arg Cys Val Arg			
340	345	350	
cgt ttc ggc ggg acg cag tgt gtc tgg tct tat gag atg cag cag ctg		1104	
Arg Phe Gly Gly Thr Gln Cys Val Trp Ser Tyr Glu Met Gln Gln Leu			
355	360	365	
ttc cat gaa aac tac gaa cac aat cgc aag ggt tac atc caa gac ctc		1152	

Phe His Glu Asn Tyr Glu His Asn Arg Lys Gly Tyr Ile Gln Asp Leu			
370	375	380	
cac aac agc aaa atc cac gca gcc atc acg ctc cat ccg aac aaa agg			1200
His Asn Ser Lys Ile His Ala Ala Ile Thr Leu His Pro Asn Lys Arg			
385	390	395	400
ccc gcg tac cag tac aga ctt cat aac tac atg ctc agc cgc aag atc			1248
Pro Ala Tyr Gln Tyr Arg Leu His Asn Tyr Met Leu Ser Arg Lys Ile			
405	410	415	
tcc gag ctc cgc tac cgc acc atc cag ctc cac cgg gag agc gct ctc			1296
Ser Glu Leu Arg Tyr Arg Thr Ile Gln Leu His Arg Glu Ser Ala Leu			
420	425	430	
atg agc aag ctc agc aac agt gaa gtg agc aaa gag gac caa cag ctg			1344
Met Ser Lys Leu Ser Asn Ser Glu Val Ser Lys Glu Asp Gln Gln Leu			
435	440	445	
gga agg acg ccg tcc ttc aac cac ttc cag cct cgg gag aga aat gaa			1392
Gly Arg Thr Pro Ser Phe Asn His Phe Gln Pro Arg Glu Arg Asn Glu			
450	455	460	
gtc atg gag tgg gag ttc ctg acg ggg aag ctg ctt tac tca gct gca			1440
Val Met Glu Trp Glu Phe Leu Thr Gly Lys Leu Leu Tyr Ser Ala Ala			
465	470	475	480
gag aac cag cct cct cga cag agc atc aac agc atc cta agg tca gct			1488
Glu Asn Gln Pro Pro Arg Gln Ser Ile Asn Ser Ile Leu Arg Ser Ala			
485	490	495	
ctg gat gac act gtc ctg cag gtg atg gag atg atc aac gag aat gcc			1536
Leu Asp Asp Thr Val Leu Gln Val Met Glu Met Ile Asn Glu Asn Ala			
500	505	510	
aag agt agg ggc cga ctc atc gac ttc aag gaa att cag tat ggc tac			1584
Lys Ser Arg Gly Arg Leu Ile Asp Phe Lys Glu Ile Gln Tyr Gly Tyr			
515	520	525	
cgc agg gtt gat ccc atg cac ggg gtt gag tac ata ttg gac ctg cta			1632
Arg Arg Val Asp Pro Met His Gly Val Glu Tyr Ile Leu Asp Leu Leu			
530	535	540	
ctc ctg tac aaa agg cac aaa gga agg aaa ctg act gtg cct gtg agg			1680
Leu Leu Tyr Lys Arg His Lys Gly Arg Lys Leu Thr Val Pro Val Arg			
545	550	555	560
cgc cat gcc tat ctt cag cag cca ttt agc aag cct ttc ttc aga gag			1728
Arg His Ala Tyr Leu Gln Gln Pro Phe Ser Lys Pro Phe Phe Arg Glu			

565	570	575	
gtg gaa gaa ctc gac gtc aac cgt ctg gtg gag agt atc aac agc ggt			1776
Val Glu Glu Leu Asp Val Asn Arg Leu Val Glu Ser Ile Asn Ser Gly			
580	585	590	
aca cag tca ttc tcc gtt ata tcc aat tct cta aaa att ctc tct tct			1824
Thr Gln Ser Phe Ser Val Ile Ser Asn Ser Leu Lys Ile Leu Ser Ser			
595	600	605	
ctt caa gag gcc aaa gac ata gga ggg cac aat gaa aag aaa gta cac			1872
Leu Gln Glu Ala Lys Asp Ile Gly Gly His Asn Glu Lys Lys Val His			
610	615	620	
att ctc gtt cca ctc gtt gga agg tac gac att ttc ttg aga ttc atg			1920
Ile Leu Val Pro Leu Val Gly Arg Tyr Asp Ile Phe Leu Arg Phe Met			
625	630	635	640
gaa aat ttt gaa agt acg tgt ctt atc cca aag caa aat gtc aag ctt			1968
Glu Asn Phe Glu Ser Thr Cys Leu Ile Pro Lys Gln Asn Val Lys Leu			
645	650	655	
gtc atc atc ctt ttc agc agg gat gct ggc caa gag tcc atc aag cac			2016
Val Ile Ile Leu Phe Ser Arg Asp Ala Gly Gln Glu Ser Ile Lys His			
660	665	670	
att gag ctg ata caa gaa tat cag agc agg tat ccc agt gca gaa atg			2064
Ile Glu Leu Ile Gln Glu Tyr Gln Ser Arg Tyr Pro Ser Ala Glu Met			
675	680	685	
atg ctc att ccc atg aag gga gag ttt tcc aga ggt ctt ggt ctt gaa			2112
Met Leu Ile Pro Met Lys Gly Glu Phe Ser Arg Gly Leu Gly Leu Glu			
690	695	700	
atg gct tct tcc cag ttt gac aat gac aca ttg ctg cta ttt tgt gat			2160
Met Ala Ser Ser Gln Phe Asp Asn Asp Thr Leu Leu Leu Phe Cys Asp			
705	710	715	720
gtt gac ttg att ttc aga gga gac ttc ctc caa cgc tgt cga gac aat			2208
Val Asp Leu Ile Phe Arg Gly Asp Phe Leu Gln Arg Cys Arg Asp Asn			
725	730	735	
aca gtt cag gga caa cag gta tat tac ccc atc atc ttt agc cag tat			2256
Thr Val Gln Gly Gln Gln Val Tyr Tyr Pro Ile Ile Phe Ser Gln Tyr			
740	745	750	
gac cca aag gtc acc cat atg aga aat cct ccc aca gag ggt gac ttt			2304
Asp Pro Lys Val Thr His Met Arg Asn Pro Pro Thr Glu Gly Asp Phe			
755	760	765	

gtat ttc tca aag gaa act ggg ttt tgg aga gac tat ggc tac gga atc			2352
Val Phe Ser Lys Glu Thr Gly Phe Trp Arg Asp Tyr Gly Tyr Gly Ile			
770	775	780	
aca tgc att tac aaa agc gat cta ctg ggt gca ggt gga ttt gat acc			2400
Thr Cys Ile Tyr Lys Ser Asp Leu Leu Gly Ala Gly Gly Phe Asp Thr			
785	790	795	800
tca ata caa ggc tgg gga ctg gaa gat gta gat ctc tat aat aaa gtc			2448
Ser Ile Gln Gly Trp Gly Leu Glu Asp Val Asp Leu Tyr Asn Lys Val			
805	810	815	
atc cta tct ggc tta cgg ccc ttc aga agt caa gaa gtg gga gtg gtg			2496
Ile Leu Ser Gly Leu Arg Pro Phe Arg Ser Gln Glu Val Gly Val Val			
820	825	830	
cat att ttc cat cct gtt cat tgt gat cct aac ttg gac cct aag cag			2544
His Ile Phe His Pro Val His Cys Asp Pro Asn Leu Asp Pro Lys Gln			
835	840	845	
tat aag atg tgc tta gga tcc aaa gca agt act ttt gcc tca acc atg			2592
Tyr Lys Met Cys Leu Gly Ser Lys Ala Ser Thr Phe Ala Ser Thr Met			
850	855	860	
caa ctg gct gaa ctc tgg tta gaa aaa cat ttg ggt gtc agg gat aat			2640
Gln Leu Ala Glu Leu Trp Leu Glu Lys His Leu Gly Val Arg Asp Asn			
865	870	875	880
cga act ctc tcc			2652
Arg Thr Leu Ser			

<210> 66

<211> 884

<212> PRT

<213> mouse

<400> 66

Met Ala Val Arg Ser Arg Arg Pro Trp Val Ser Val Ala Leu Gly Leu			
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Val Leu Gly Phe Thr Ala Ala Ser Trp Leu Ile Ala Pro Arg Val Ala			
20	25	30	

Glu Leu Ser Glu Lys Arg Arg Arg Gly Ser Ser Leu Cys Ser Tyr Tyr
35 40 45

Gly Arg Ser Ala Thr Gly Pro Arg Ala Asp Ala Gln Gln Leu Leu Pro
50 55 60

Gln Pro Gln Ser Arg Pro Arg Leu Glu Gln Ser Pro Pro Pro Ala Ser
65 70 75 80

His Glu Leu Pro Gly Pro Gln Gln Pro Glu Ala Ala Pro Gly Gly Pro
85 90 95

Ser Phe Arg Ser Ser Pro Trp Gln Gln Pro Ala Leu Leu Pro Gln Arg
100 105 110

Arg Arg Gly His Thr Pro Glu Gly Ala Thr Ala Leu Pro Gly Ala Pro
115 120 125

Ala Ala Lys Gly Glu Pro Glu Glu Asp Gly Gly Ala Ala Asp Pro
130 135 140

Arg Lys Gly Gly Arg Pro Gly Ser Ser His Asn Gly Ser Gly Asp Gly
145 150 155 160

Gly Ala Ala Val Pro Thr Ser Gly Pro Gly Asp Phe Leu Tyr Val Gly
165 170 175

Val Met Thr Ala Gln Lys Tyr Leu Gly Ser Arg Ala Leu Ala Ala Gln
180 185 190

Arg Thr Trp Ala Arg Phe Ile Pro Gly Arg Val Glu Phe Phe Ser Ser
195 200 205

Gln Gln Ser Pro Ser Ala Ala Leu Gly Gln Pro Pro Pro Pro Leu Pro
210 215 220

Val Ile Ala Leu Pro Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys
225 230 235 240

Ser Phe Met Met Ile Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr
245 250 255

Glu Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Lys
260 265 270

Leu Glu Glu Phe Leu Arg Ser Leu Asn Ser Ser Lys Pro Leu Tyr Leu
275 280 285

Gly Gln Thr Gly Leu Gly Asn Thr Glu Glu Leu Gly Lys Leu Gly Leu
290 295 300

Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Met Ile Phe Ser
305 310 315 320

Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly Glu Cys Leu Arg
 325 330 335

Glu Met Tyr Thr Thr His Glu Asp Val Glu Val Gly Arg Cys Val Arg
 340 345 350

Arg Phe Gly Gly Thr Gln Cys Val Trp Ser Tyr Glu Met Gln Gln Leu
355 360 365

Phe His Glu Asn Tyr Glu His Asn Arg Lys Gly Tyr Ile Gln Asp Leu
 370 375 380

His Asn Ser Lys Ile His Ala Ala Ile Thr Leu His Pro Asn Lys Arg
385 390 395 400

Pro Ala Tyr Gln Tyr Arg Leu His Asn Tyr Met Leu Ser Arg Lys Ile
405 410 415

Met Ser Lys Leu Ser Asn Ser Glu Val Ser Lys Glu Asp Gln Gln Leu
435 440 445

Val Met Glu Trp Glu Phe Leu Thr Gly Lys Leu Leu Tyr Ser Ala Ala

465 470 475 480

Glu Asn Gln Pro Pro Arg Gln Ser Ile Asn Ser Ile Leu Arg Ser Ala
485 490 495

Leu Asp Asp Thr Val Leu Gln Val Met Glu Met Ile Asn Glu Asn Ala
500 505 510

Lys Ser Arg Gly Arg Leu Ile Asp Phe Lys Glu Ile Gln Tyr Gly Tyr
515 520 525

Arg Arg Val Asp Pro Met His Gly Val Glu Tyr Ile Leu Asp Leu Leu
530 535 540

Leu Leu Tyr Lys Arg His Lys Gly Arg Lys Leu Thr Val Pro Val Arg
545 550 555 560

Arg His Ala Tyr Leu Gln Gln Pro Phe Ser Lys Pro Phe Phe Arg Glu
565 570 575

Val Glu Glu Leu Asp Val Asn Arg Leu Val Glu Ser Ile Asn Ser Gly
580 585 590

Thr Gln Ser Phe Ser Val Ile Ser Asn Ser Leu Lys Ile Leu Ser Ser
595 600 605

Leu Gln Glu Ala Lys Asp Ile Gly Gly His Asn Glu Lys Lys Val His
610 615 620

Ile Leu Val Pro Leu Val Gly Arg Tyr Asp Ile Phe Leu Arg Phe Met
625 630 635 640

Glu Asn Phe Glu Ser Thr Cys Leu Ile Pro Lys Gln Asn Val Lys Leu
645 650 655

Val Ile Ile Leu Phe Ser Arg Asp Ala Gly Gln Glu Ser Ile Lys His
660 665 670

Ile Glu Leu Ile Gln Glu Tyr Gln Ser Arg Tyr Pro Ser Ala Glu Met
675 680 685

Met Leu Ile Pro Met Lys Gly Glu Phe Ser Arg Gly Leu Gly Leu Glu
690 695 700

Met Ala Ser Ser Gln Phe Asp Asn Asp Thr Leu Leu Leu Phe Cys Asp
705 710 715 720

Val Asp Leu Ile Phe Arg Gly Asp Phe Leu Gln Arg Cys Arg Asp Asn
725 730 735

Thr Val Gln Gly Gln Gln Val Tyr Tyr Pro Ile Ile Phe Ser Gln Tyr
740 745 750

Asp Pro Lys Val Thr His Met Arg Asn Pro Pro Thr Glu Gly Asp Phe
755 760 765

Val Phe Ser Lys Glu Thr Gly Phe Trp Arg Asp Tyr Gly Tyr Gly Ile
770 775 780

Thr Cys Ile Tyr Lys Ser Asp Leu Leu Gly Ala Gly Gly Phe Asp Thr
785 790 795 800

Ser Ile Gln Gly Trp Gly Leu Glu Asp Val Asp Leu Tyr Asn Lys Val
805 810 815

Ile Leu Ser Gly Leu Arg Pro Phe Arg Ser Gln Glu Val Gly Val Val
820 825 830

His Ile Phe His Pro Val His Cys Asp Pro Asn Leu Asp Pro Lys Gln
835 840 845

Tyr Lys Met Cys Leu Gly Ser Lys Ala Ser Thr Phe Ala Ser Thr Met
850 855 860

Gln Leu Ala Glu Leu Trp Leu Glu Lys His Leu Gly Val Arg Asp Asn
865 870 875 880

Arg Thr Leu Ser

<210> 67
<211> 2490
<212> DNA
<213> mouse

<220>

<221> CDS

<222> (1)..(2325)

<223>

<400> 67

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1				5			10			15						
gcc	gtg	ggc	atc	tct	ctg	ggc	ttc	acc	ctg	agc	ctg	ctc	agc	gtc	acc	96
Ala	Val	Gly	Ile	Ser	Leu	Gly	Phe	Thr	Leu	Ser	Leu	Leu	Ser	Val	Thr	
			20				25			30						
tgg	gtg	gag	gag	cct	tgc	gga	ccc	ggg	ccg	ccc	caa	ccc	gga	gac	ict	144
Trp	Val	Glu	Glu	Pro	Cys	Gly	Pro	Gly	Pro	Pro	Gln	Pro	Gly	Asp	Ser	
			35				40			45						
gag	ctg	ccg	ccg	ccg	ggc	aac	acc	aac	gcg	gcg	ccg	ccg	ccc	aac	tcg	192
Glu	Leu	Pro	Pro	Arg	Gly	Asn	Thr	Asn	Ala	Ala	Arg	Arg	Pro	Asn	Ser	
			50				55			60						
gtg	cag	ccc	gga	tcc	gag	ccg	gag	agg	ccc	ggg	gcc	ggc	gca	ggc	acc	240
Val	Gln	Pro	Gly	Ser	Glu	Arg	Glu	Arg	Pro	Gly	Ala	Gly	Ala	Gly	Thr	
			65				70			75			80			
ggt	gag	agc	tgg	gag	cct	cgt	gtc	tig	ccc	tac	cat	ccc	gcg	cag	cca	288
Gly	Glu	Ser	Trp	Glu	Pro	Arg	Val	Leu	Pro	Tyr	His	Pro	Ala	Gln	Pro	
							85			90			95			
ggc	cag	gcc	acc	aag	aag	gcc	gtc	aga	act	cg	tat	atc	agc	acg	gag	336
Gly	Gln	Ala	Thr	Lys	Lys	Ala	Val	Arg	Thr	Arg	Tyr	Ile	Ser	Thr	Glu	
							100			105			110			
ctg	ggc	atc	agg	cag	aag	ctt	ctg	gtg	gca	gtg	ctg	acc	tca	caa	gcc	384
Leu	Gly	Ile	Arg	Gln	Lys	Leu	Leu	Val	Ala	Val	Leu	Thr	Ser	Gln	Ala	
							115			120			125			
acg	tig	cct	aca	ctg	ggt	gtg	gt	gt	aa	ac	ct	ctg	gga	cac	cga	432
Thr	Leu	Pro	Thr	Leu	Gly	Val	Ala	Val	Asn	Arg	Thr	Leu	Gly	His	Arg	
							130			135			140			
ctg	gag	cat	gt	gt	gt	ttc	ctg	acc	ggt	g	gg	ggc	ccg	aca	cct	480
Leu	Glu	His	Val	Val	Phe	Leu	Thr	Gly	Ala	Arg	Gly	Arg	Arg	Thr	Pro	
							145			150			155		160	

tca ggc atg gcg gtg gtg gca ctg ggc gaa gag agg ccc atc gga cac			528
Ser Gly Met Ala Val Val Ala Leu Gly Glu Glu Arg Pro Ile Gly His			
165	170	175	
ctg cac ctg gcg ctg cgc cac ctg ctg gag caa cac ggc gat gac ttt			576
Leu His Leu Ala Leu Arg His Leu Leu Glu Gln His Gly Asp Asp Phe			
180	185	190	
gac tgg ttt ttc cta gtg cct gat gcc acc tat act gaa gcg cat gga			624
Asp Trp Phe Phe Leu Val Pro Asp Ala Thr Tyr Thr Glu Ala His Gly			
195	200	205	
ctg gac cgc cta gct ggc cac ctc agc ctt gct tca gca acc cat ctc			672
Leu Asp Arg Leu Ala Gly His Leu Ser Leu Ala Ser Ala Thr His Leu			
210	215	220	
tat ctt ggc cg ^g ccg cag gac ttc atc ggt gga gat act acc cca ggc			720
Tyr Leu Gly Arg Pro Gln Asp Phe Ile Gly Gly Asp Thr Thr Pro Gly			
225	230	235	240
cgc tac tgc cac ggg ggc ttt gga gtc ttg ctc tct cgc aca ctg cta			768
Arg Tyr Cys His Gly Gly Phe Gly Val Leu Leu Ser Arg Thr Leu Leu			
245	250	255	
cag caa ctg cgc ccc cac ctg gaa agc tgc cgc aac gac atc gtc agt			816
Gln Gln Leu Arg Pro His Leu Glu Ser Cys Arg Asn Asp Ile Val Ser			
260	265	270	
gct cgc ccg gat gag tgg ttg ggc cgc tgc atc ctt gat gcc aca ggc			864
Ala Arg Pro Asp Glu Trp Leu Gly Arg Cys Ile Leu Asp Ala Thr Gly			
275	280	285	
gtg ggc tgt act ggt gac cac gag gga atg cac tac aac tac ctg gaa			912
Val Gly Cys Thr Gly Asp His Glu Gly Met His Tyr Asn Tyr Leu Glu			
290	295	300	
ctg agc ccc ggg gag cct gta cag gag ggg gac cct cgt ttc cgc agc			960
Leu Ser Pro Gly Glu Pro Val Gln Glu Gly Asp Pro Arg Phe Arg Ser			
305	310	315	320
gcc ttg aca gcc cat ccc gtg cgt gac cct gtg cac atg tac cag ctg			1008
Ala Leu Thr Ala His Pro Val Arg Asp Pro Val His Met Tyr Gln Leu			
325	330	335	
cac aaa gct ttt gcc cgc gct gag ctg gac cgc acg tac cag gag att			1056
His Lys Ala Phe Ala Arg Ala Glu Leu Asp Arg Thr Tyr Gln Glu Ile			
340	345	350	
caa gaa ttg cag tgg gag atc cag aat acc agc cga ctg gct gct gat			1104

Gln Glu Leu Gln Trp Glu Ile Gln Asn Thr Ser Arg Leu Ala Ala Asp			
355	360	365	
ggg gag aga gcc tct gcc tgg cca gtg ggc atc cca gca ccg tct cgc			1152
Gly Glu Arg Ala Ser Ala Trp Pro Val Gly Ile Pro Ala Pro Ser Arg			
370	375	380	
cct gcc tca cgc ttt gag gtt ctg cgc tgg gac tac ttc aca gaa caa			1200
Pro Ala Ser Arg Phe Glu Val Leu Arg Trp Asp Tyr Phe Thr Glu Gln			
385	390	395	400
tac gcg ttc tcc tgc gcc gat ggc tct ccc cgc tgc ccg ttg cgt ggg			1248
Tyr Ala Phe Ser Cys Ala Asp Gly Ser Pro Arg Cys Pro Leu Arg Gly			
405	410	415	
gcc gac cag gct gat gtg gct gac gtc ctg ggg aca gca tta gag gag			1296
Ala Asp Gln Ala Asp Val Ala Asp Val Leu Gly Thr Ala Leu Glu Glu			
420	425	430	
ctc aac cgc cgt tac cag cca gcg ctg cag ctc cag aag caa cag ctg			1344
Leu Asn Arg Arg Tyr Gln Pro Ala Leu Gln Leu Lys Gln Gln Leu			
435	440	445	
gtg aac ggc tac cgg cgt ttt gat cca gcc cga ggc atg gag tac aca			1392
Val Asn Gly Tyr Arg Arg Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr			
450	455	460	
cta gac ctg cag ctg gaa gcg ctg aca ccc cag ggt ggc cgc tgg ccc			1440
Leu Asp Leu Gln Leu Glu Ala Leu Thr Pro Gln Gly Gly Arg Trp Pro			
465	470	475	480
ctc acc cgc agg gtg cag ctc ctt cgg ccc ttg agc cga gtg gag atc			1488
Leu Thr Arg Arg Val Gln Leu Leu Arg Pro Leu Ser Arg Val Glu Ile			
485	490	495	
ttg cct gta ccc tat gtc acc gag gct tct cgg ctc act gtg cta ctg			1536
Leu Pro Val Pro Tyr Val Thr Glu Ala Ser Arg Leu Thr Val Leu Leu			
500	505	510	
ccg ctg gct gca gcg gaa cga gac ctg gct tct ggc ttc tta gaa gcc			1584
Pro Leu Ala Ala Ala Glu Arg Asp Leu Ala Ser Gly Phe Leu Glu Ala			
515	520	525	
ttt gcc act gca gcc ctg gaa cct ggt gat gca gca gcc ttg acc ctg			1632
Phe Ala Thr Ala Ala Leu Glu Pro Gly Asp Ala Ala Leu Thr Leu			
530	535	540	
ctg ctg ctg tat gag cca cgc cag gcc cag cgg gca gcc cac tca gac			1680
Leu Leu Leu Tyr Glu Pro Arg Gln Ala Gln Arg Ala Ala His Ser Asp			

545	550	555	560
gtc ttc gca cct gtc aag gcc cac gig gca gag cta gag cgg cgt ttc			1728
Val Phe Ala Pro Val Lys Ala His Val Ala Glu Leu Glu Arg Arg Phe			
565	570	575	
cct ggt gcc cggt gtg ccc tgg ctc agt gtg cag aca gca gcg ccc tct			1776
Pro Gly Ala Arg Val Pro Trp Leu Ser Val Gln Thr Ala Ala Pro Ser			
580	585	590	
cca ctg cgt ctc atg gat ctg ctg tcc aag aag cac cca cta gac act			1824
Pro Leu Arg Leu Met Asp Leu Leu Ser Lys Lys His Pro Leu Asp Thr			
595	600	605	
ctg ttc ctg ctg gcc ggg cca gac acg gta ctc aca cct gat ttc ctg			1872
Leu Phe Leu Leu Ala Gly Pro Asp Thr Val Leu Thr Pro Asp Phe Leu			
610	615	620	
aac cgc tgc cgc atg cat gcc atc tct ggc tgg cag gcc ttc ttc ccc			1920
Asn Arg Cys Arg Met His Ala Ile Ser Gly Trp Gln Ala Phe Phe Pro			
625	630	635	640
atg cac ttc cag gcc ttc cac cct gct gtg gct cct cct cag ggc cct			1968
Met His Phe Gln Ala Phe His Pro Ala Val Ala Pro Pro Gln Gly Pro			
645	650	655	
ggg cca cca gag ctg ggc cgt gac acc ggt cac ttt gat cgc cag gct			2016
Gly Pro Pro Glu Leu Gly Arg Asp Thr Gly His Phe Asp Arg Gln Ala			
660	665	670	
gcc agt gag gca tgc ttc tac aac tcc gac tat gtg gcg gcc cgt ggc			2064
Ala Ser Glu Ala Cys Phe Tyr Asn Ser Asp Tyr Val Ala Ala Arg Gly			
675	680	685	
cgg ctg gtg gcg gcc tcg gag cag gag gag ctg ctg gag agc ctg			2112
Arg Leu Val Ala Ala Ser Glu Gln Glu Glu Glu Leu Leu Glu Ser Leu			
690	695	700	
gat gtg tac gag ttg ttt ctg cgc ttc tcc aac ttg cac gtg ctg aga			2160
Asp Val Tyr Glu Leu Phe Leu Arg Phe Ser Asn Leu His Val Leu Arg			
705	710	715	720
gca gta gag cca gcc ttg ctg cag cgc tac cgg gcc cag ccg tgc agt			2208
Ala Val Glu Pro Ala Leu Leu Gln Arg Tyr Arg Ala Gln Pro Cys Ser			
725	730	735	
gca cgg ctc agt gaa gac cit tac cac cgc tgc cgc cag agc gta ctt			2256
Ala Arg Leu Ser Glu Asp Leu Tyr His Arg Cys Arg Gln Ser Val Leu			
740	745	750	

gag ggc ctt ggc tcc cgc acc cag ctt gcc atg ctg ctc ttt gag cag 2304
Glu Gly Leu Gly Ser Arg Thr Gln Leu Ala Met Leu Leu Phe Glu Gln
755 760 765

gaa cag ggg aac agc acc taa gccccgtcac ctgtccctgc tcitccccag 2355
Glu Gln Gly Asn Ser Thr
770

gaacctggag ccacgtgccca gcctcgctgg acagggttgg ctgttagccctc agtccctagg 2415
gcagcccaact ggcccttgtt ctcttgcttt ttggaccctt tgggttcagg acaagccctg 2475
agacagatgc cctag 2490

<210> 68

<211> 774

<212> PRT

<213> mouse

<400> 68

Met Arg Ala Ser Leu Leu Leu Ser Val Leu Arg Pro Ala Gly Pro Val
1 5 10 15

Ala Val Gly Ile Ser Leu Gly Phe Thr Leu Ser Leu Leu Ser Val Thr
20 25 30

Trp Val Glu Glu Pro Cys Gly Pro Gly Pro Pro Gln Pro Gly Asp Ser
35 40 45

Glu Leu Pro Pro Arg Gly Asn Thr Asn Ala Ala Arg Arg Pro Asn Ser
50 55 60

Val Gln Pro Gly Ser Glu Arg Glu Arg Pro Gly Ala Gly Ala Gly Thr
65 70 75 80

Gly Glu Ser Trp Glu Pro Arg Val Leu Pro Tyr His Pro Ala Gln Pro
 85 90 95

Gly Gln Ala Thr Lys Lys Ala Val Arg Thr Arg Tyr Ile Ser Thr Glu
 100 105 110

Leu Gly Ile Arg Gln Lys Leu Leu Val Ala Val Leu Thr Ser Gln Ala
115 120 125

Thr Leu Pro Thr Leu Gly Val Ala Val Asn Arg Thr Leu Gly His Arg
130 135 140

Leu Glu His Val Val Phe Leu Thr Gly Ala Arg Gly Arg Arg Thr Pro
145 150 155 160

Ser Gly Met Ala Val Val Ala Leu Gly Glu Glu Arg Pro Ile Gly His
 165 170 175

Asp Trp Phe Phe Leu Val Pro Asp Ala Thr Tyr Thr Glu Ala His Gly
195 200 205

Leu Asp Arg Leu Ala Gly His Leu Ser Leu Ala Ser Ala Thr His Leu
210 215 220

Tyr Leu Gly Arg Pro Gln Asp Phe Ile Gly Gly Asp Thr Thr Pro Gly

225 230 235 240

Arg Tyr Cys His Gly Gly Phe Gly Val Leu Leu Ser Arg Thr Leu Leu
245 250 255

Gln Gln Leu Arg Pro His Leu Glu Ser Cys Arg Asn Asp Ile Val Ser
260 265 270

Ala Arg Pro Asp Glu Trp Leu Gly Arg Cys Ile Leu Asp Ala Thr Gly
275 280 285

Val Gly Cys Thr Gly Asp His Glu Gly Met His Tyr Asn Tyr Leu Glu
290 295 300

Leu Ser Pro Gly Glu Pro Val Gln Glu Gly Asp Pro Arg Phe Arg Ser
305 310 315 320

Ala Leu Thr Ala His Pro Val Arg Asp Pro Val His Met Tyr Gln Leu
325 330 335

His Lys Ala Phe Ala Arg Ala Glu Leu Asp Arg Thr Tyr Gln Glu Ile
340 345 350

Gln Glu Leu Gln Trp Glu Ile Gln Asn Thr Ser Arg Leu Ala Ala Asp
355 360 365

Gly Glu Arg Ala Ser Ala Trp Pro Val Gly Ile Pro Ala Pro Ser Arg
370 375 380

Pro Ala Ser Arg Phe Glu Val Leu Arg Trp Asp Tyr Phe Thr Glu Gln
385 390 395 400

Tyr Ala Phe Ser Cys Ala Asp Gly Ser Pro Arg Cys Pro Leu Arg Gly
405 410 415

Ala Asp Gln Ala Asp Val Ala Asp Val Leu Gly Thr Ala Leu Glu Glu
420 425 430

Leu Asn Arg Arg Tyr Gln Pro Ala Leu Gln Leu Gln Lys Gln Gln Leu
435 440 445

Val Asn Gly Tyr Arg Arg Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr
450 455 460

Leu Asp Leu Gln Leu Glu Ala Leu Thr Pro Gln Gly Gly Arg Trp Pro
465 470 475 480

Leu Thr Arg Arg Val Gln Leu Leu Arg Pro Leu Ser Arg Val Glu Ile
485 490 495

Leu Pro Val Pro Tyr Val Thr Glu Ala Ser Arg Leu Thr Val Leu Leu
500 505 510

Pro Leu Ala Ala Ala Glu Arg Asp Leu Ala Ser Gly Phe Leu Glu Ala
515 520 525

Phe Ala Thr Ala Ala Leu Glu Pro Gly Asp Ala Ala Ala Leu Thr Leu
530 535 540

Leu Leu Leu Tyr Glu Pro Arg Gln Ala Gln Arg Ala Ala His Ser Asp
545 550 555 560

Val Phe Ala Pro Val Lys Ala His Val Ala Glu Leu Glu Arg Arg Phe
565 570 575

Pro Gly Ala Arg Val Pro Trp Leu Ser Val Gln Thr Ala Ala Pro Ser
580 585 590

Pro Leu Arg Leu Met Asp Leu Leu Ser Lys Lys His Pro Leu Asp Thr
595 600 605

Leu Phe Leu Leu Ala Gly Pro Asp Thr Val Leu Thr Pro Asp Phe Leu
610 615 620

Asn Arg Cys Arg Met His Ala Ile Ser Gly Trp Gln Ala Phe Phe Pro
625 630 635 640

Met His Phe Gln Ala Phe His Pro Ala Val Ala Pro Pro Gln Gly Pro
645 650 655

Gly Pro Pro Glu Leu Gly Arg Asp Thr Gly His Phe Asp Arg Gln Ala
660 665 670

Ala Ser Glu Ala Cys Phe Tyr Asn Ser Asp Tyr Val Ala Ala Arg Gly
675 680 685

Arg Leu Val Ala Ala Ser Glu Gln Glu Glu Glu Leu Leu Glu Ser Leu
690 695 700

Asp Val Tyr Glu Leu Phe Leu Arg Phe Ser Asn Leu His Val Leu Arg
705 710 715 720

Ala Val Glu Pro Ala Leu Leu Gln Arg Tyr Arg Ala Gln Pro Cys Ser
725 730 735

Ala Arg Leu Ser Glu Asp Leu Tyr His Arg Cys Arg Gln Ser Val Leu
740 745 750

Glu Gly Leu Gly Ser Arg Thr Gln Leu Ala Met Leu Leu Phe Glu Gln
755 760 765

Glu Gln Gly Asn Ser Thr
770

<210> 69
<211> 984
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (1)..(984)
<223>

<400> 69

atg ttg ccc tcc cgg agg aaa gcg gcg cag ctg ccc tgg gag gat ggc	48
Met Leu Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp Gly	
1 5 10 15	
agg gcc agg ttg ctt cct gga ggc ctc cgc cgg aaa tgc tcc atc ttc	96
Arg Ala Arg Leu Leu Pro Gly Gly Leu Arg Arg Lys Cys Ser Ile Phe	
20 25 30	
cac cic ttc att gcc ttt ctc ctc ttc ttc tcc ctg ctc tgg	144
His Leu Phe Ile Ala Phe Leu Leu Val Phe Phe Ser Leu Leu Trp	
35 40 45	
ctg cag ctc agc tgt tct gga gat atg gcc cag gtg acc agg gga caa	192
Leu Gln Leu Ser Cys Ser Gly Asp Met Ala Gln Val Thr Arg Gly Gln	
50 55 60	
ggg caa gag acc tcg ggt cca ccc cgg gct tgc cct cca gag ccg ccc	240
Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys Pro Pro Glu Pro Pro	
65 70 75 80	
cct gag cac tgg gaa gaa gat gag tcc tgg ggg ccc cac cgc ttc gca	288
Pro Glu His Trp Glu Glu Asp Glu Ser Trp Gly Pro His Arg Leu Ala	
85 90 95	
gtg ctc gtg ccc ttt cgt gag cgc ttt gag gag ctg ctg gtc ttt gtg	336
Val Leu Val Pro Phe Arg Glu Arg Phe Glu Glu Leu Leu Val Phe Val	
100 105 110	
ccc cac atg cac cgc ttc cta agc agg aag agg atc cag cac cac atc	384
Pro His Met His Arg Phe Leu Ser Arg Lys Arg Ile Gln His His Ile	
115 120 125	
tat gtg ctc aac cag gtg gac cat ttc agg ttc aat cgg gca gca ctc	432
Tyr Val Leu Asn Gln Val Asp His Phe Arg Phe Asn Arg Ala Ala Leu	
130 135 140	
atc aat gtg ggc ttc ctg gag agc agc aac agc aca gac tac atc gcc	480
Ile Asn Val Gly Phe Leu Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala	
145 150 155 160	
atg cac gat gtg gac ctg ctc cct ctc aat gag gag ctg gac tat ggc	528
Met His Asp Val Asp Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly	
165 170 175	
ttc ccg gag gct ggg ccc ttc cat gtg gcc tcc cca gag ctc cac cct	576
Phe Pro Glu Ala Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro	

180	185	190	
c tc tac cac tac aag acc tat gtg ggc ggc att ctg ctg ctg tcc aaa			624
Leu Tyr His Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Ser Lys			
195	200	205	
c ag cac tac cag ctg tgc aac gga atg tcc aac cgc ttt tgg ggc tgg			672
Gln His Tyr Gln Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp			
210	215	220	
ggc c ga gag gat gat gaa ttc tac cgg cgc atc aaa gga gct ggc c tc			720
Gly Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu			
225	230	235	240
c ag c tt ttc cgc ccc tcg gga atc aca act ggg tac cag aca ttt cgc			768
Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Gln Thr Phe Arg			
245	250	255	
c ac t tg cat gac cct gcc tgg cgg aag agg gac caa aaa cgc att gcg			816
His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg Ile Ala			
260	265	270	
gct c aa aaa c ag gaa c ag ttc aag gtg gac cgg gag gga ggc ctg aac			864
Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly Gly Leu Asn			
275	280	285	
act gtg aag tac cgg gtg gat tcc cgc acg gca ctg tct ata gga ggg			912
Thr Val Lys Tyr Arg Val Asp Ser Arg Thr Ala Leu Ser Ile Gly Gly			
290	295	300	
gcc ccg tgc act gtc ctc aat gtc atg ctg gac tgc gat aaa aca gcc			960
Ala Pro Cys Thr Val Leu Asn Val Met Leu Asp Cys Asp Lys Thr Ala			
305	310	315	320
acc cca tgg tgc ata ttt ggc tga			984
Thr Pro Trp Cys Ile Phe Gly			
325			

<210> 70
 <211> 327
 <212> PRT
 <213> mouse

 <400> 70

Met Leu Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp Gly

1

5

10

15

Arg Ala Arg Leu Leu Pro Gly Gly Leu Arg Arg Lys Cys Ser Ile Phe
20 25 30

His Leu Phe Ile Ala Phe Leu Leu Leu Val Phe Phe Ser Leu Leu Trp
35 40 45

Leu Gln Leu Ser Cys Ser Gly Asp Met Ala Gln Val Thr Arg Gly Gln
50 55 60

Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys Pro Pro Glu Pro Pro
65 70 75 80

Pro Glu His Trp Glu Glu Asp Glu Ser Trp Gly Pro His Arg Leu Ala
85 90 95

Val Leu Val Pro Phe Arg Glu Arg Phe Glu Glu Leu Leu Val Phe Val
100 105 110

Pro His Met His Arg Phe Leu Ser Arg Lys Arg Ile Gln His His Ile
115 120 125

Tyr Val Leu Asn Gln Val Asp His Phe Arg Phe Asn Arg Ala Ala Leu
130 135 140

Ile Asn Val Gly Phe Leu Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala
145 150 155 160

Met His Asp Val Asp Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly
165 170 175

Phe Pro Glu Ala Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro
180 185 190

Leu Tyr His Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys
195 200 205

Gln His Tyr Gln Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp
210 215 220

Gly Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu
225 230 235 240

Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Gln Thr Phe Arg
245 250 255

His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg Ile Ala
260 265 270

Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly Gly Leu Asn
275 280 285

Thr Val Lys Tyr Arg Val Asp Ser Arg Thr Ala Leu Ser Ile Gly Gly
290 295 300

Ala Pro Cys Thr Val Leu Asn Val Met Leu Asp Cys Asp Lys Thr Ala
305 310 315 320

Thr Pro Trp Cys Ile Phe Gly
325